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YBC522Mu01 100 μ g

Recombinant Hemopoietic Cell Kinase (HCK)

Organism Species: *Mus musculus* (Mouse)

Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY

NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

10th Edition (Revised in Jan, 2014)

[PROPERTIES]

Residues: Gly2~Pro524

Tags: Two N-terminal Tags, His-tag and T7-tag

Accession: P08103

Host: *E. coli*

Subcellular Location: Membrane; Lipid-anchor. caveola.

Lysosome. Cell projection; podosome membrane; Lipid-anchor. Cytoplasm; cytosol.

Purity: >95%

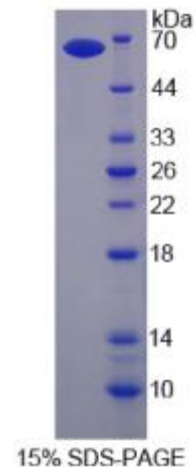
Endotoxin Level: <1.0EU per 1 μ g (determined by the LAL method).

Formulation: Supplied as lyophilized form in PBS, pH7.4, containing 5% trehalose, 0.01% sarcosyl.

Predicted isoelectric point: 6.9

Predicted Molecular Mass:

62.7kDa





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Applications: SDS-PAGE; WB; ELISA; IP.

(May be suitable for use in other assays to be determined by the end user.)

[USAGE]

Reconstitute in sterile PBS, pH7.2-pH7.4.

[STORAGE AND STABILITY]

Storage: Avoid repeated freeze/thaw cycles.

Store at 2-8°C for one month.

Aliquot and store at -80°C for 12 months.

Stability Test: The thermal stability is described by the loss rate of the target protein. The loss rate was determined by accelerated thermal degradation test, that is, incubate the protein at 37°C for 48h, and no obvious degradation and precipitation were observed. (Referring from China Biological Products Standard, which was calculated by the Arrhenius equation.) The loss of this protein is less than 5% within the expiration date under appropriate storage condition.

[SEQUENCES]

The sequence of the target protein is listed below.

GGRSSCEDP GPCRSEGRAP RMGCVKSRFL RDGSKASKTE PSANQKGPVY VPDPTSSSKL
GPNNSNSMPP GFVEGSEDTI VVALYDYEAI HREDLSFQKG DQMVVLEEAG EWWKARSLAT
KKEGYIPSNY VARVNSLETE EWWFKGISRK DAERHLLAPG NMLGSFMIRD SETTKGSYSL
SVRDFDPQHG DTVKHYKIRT LDSSGGFYISP RSTFSSLQEL VLHYKKGKDG LCQKLSVPCV
S P K P Q K P W E K D A W E I P R E S L Q M E K K L G A G Q F G E V W M A T Y N K H T K V A V K T M
KPGSMSVEAF LAEANLMKSL QHDKLVKLHA VVSQEPFIV TEFMAKGSLL DFLKSEEGSK
QPLPLIDFS AQISEGMAFI EQRNYIHRDL RAANILVSAS LVCKIADFGL ARIIEDNEYT
AREGAKFPIK WTAPEAINFG SFTIKSDVWS FGILLMEIVT YGRIPYPGMS NPEVIRALEH
GYRMPRPDNC PEELYNIMIR CWKNRPEERP TFEYIQSVLD DFYTATESQY QQQP